ON THE POSSIBILITY OF EXPLOITING INTRA-ROW CORRELATIONS TO ESTIMATE GENETIC AND ENVIRONMENTAL VARIANCE IN A PLANTATION. SUPPLEMENT: ON PARTITIONING COVARIANCE.

D. S. Robson

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Abstract

The method described in BU-401-M for separating genetic and environmental components of phenotypic variance in a row plantation can be extended to a covariance analysis which identifies the genetic and the environmental correlation between two phenotypic traits. Since the utility of the method depends on the regularity of the autocorrelation function (covariance kernel) within rows, experimental studies are needed to test the applicability of the method.

Mimeo Series, Biometrics Unit, Cornell University.

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The method described in BU-401-M for estimating the variance components σ^2_G and σ^2_E of $X = G + E$ may also be used to estimate the covariance components $\sigma_{G(x,y)}$ and $\sigma_{E(x,y)}$ of two quantitative traits $X = G_x + E_x$ and $Y = G_y + E_y$. Genetic and environmental correlations of these two traits are then also identifiable,

$$\rho_{G(x,y)} = \frac{\sigma_{G(x,y)}}{\sigma_{G(x)}\sigma_{G(y)}} \qquad \rho_{E(x,y)} = \frac{\sigma_{E(x,y)}}{\sigma_{E(x)}\sigma_{E(y)}}$$

provided, again, that an empirical law can be determined to describe the correlation between the X-trait of the first plant in a row and the Y-trait of the k^{th} plant in the same row of the plantation. If we define this environmental correlation between the i^{th} and $(i+h)^{th}$ plants in a row as the average of the two correlations

$$\bar{\rho}_{h(x,y)} = \frac{1}{2}\left[\frac{\sigma_{X_i,Y_{i+h}}}{\sigma_{E(x)}\sigma_{E(y)}} + \frac{\sigma_{X_{i+h},Y_i}}{\sigma_{E(x)}\sigma_{E(y)}}\right]$$

then

$$\mathcal{E}\left\{\frac{(X_i - X_{i+h})(Y_i - Y_{i+h})}{2}\right\} = \sigma_{G(x,y)} + \sigma_{E(x)}\sigma_{E(y)}\left(\rho_{E(x,y)} - \bar{\rho}_{h(x,y)}\right)$$

where $\bar{\rho}_{h(x,y)}$ decreases with h, approaching zero as h gets large and approaching $\rho_{E(x,y)}$ as h approaches zero. Alternatively, defining $\rho_{h(x,y)} = \bar{\rho}_{h(x,y)} / \rho_{E(x,y)}$ we obtain the expression

$$\mathcal{E}\left\{\frac{(X_i-X_{i+h})(Y_i-Y_{i+h})}{2}\right\} = \sigma_{G(x,y)} + \sigma_{E(x,y)}(1-\rho_{h(x,y)})$$

completely analagous to the earlier

$$\mathcal{E}\left\{\frac{(X_i-X_{i+h})^2}{2}\right\} = \sigma_G^2 + \sigma_E^2(1-\rho_h) \quad .$$

Similarly, from the analysis of covariance within and between clusters of k consecutive plants in a row,

$$\psi(\sigma_{k(x,y)}) = \sigma_{G(x,y)} + \sigma_{E(x,y)}(1-\rho_{h(x,y)})$$

and

$$\psi(\sigma_{E(x,y)}\bar{R}_{k(x,y)}) = \sigma_{E(x,y)}\rho_{h(x,y)}$$

as before.

The relationship between $\rho_{h(x,y)}$ and h has probably not been studied very extensively, if at all, and would therefore constitute a reasonable and potentially valuable graduate research topic in the field of plant breeding. An experimental study of this relationship might be implemented using a crop plant which can be vegetatively reproduced in order to provide a means of checking the validity of the model and the estimation method. Thus, if a plantation of NM genetically segregating plants arranged in N rows of M equally spaced plants is supplemented with n replicates of each of M randomly chosen segregates then by embedding these nM plants in a completely randomized design consisting of n rows randomly interspersed among the N segregating rows, valid estimates of genetic and environmental components can be obtained for comparison purposes. Estimates of $\sigma_{G(x,y)}$

and $\sigma_{E(x,y)}$ obtained from the completely randomized design could be compared with corresponding estimates extrapolated from the analysis of the NM segregating plants. Further supplementation by embedding a number of pure-stand rows consisting of vegetative propogates of each of a number of randomly chosen plants would provide data for intra-row correlation analysis of non-segregating plants, to permit further checks on the fine structure of the model.